```
                   RAW SEQUENCE LISTING           DATE: 12/06/2000
                   PATENT APPLICATION:  US/09/499,526     TIME: 13:17:01

                   Input Set : A:\Pto.amc
                   Output Set: N:\CRF3\12062000\I499526.raw

                   SEQUENCE LISTING
      2 (1) GENERAL INFORMATION:
      3        (i) APPLICANT: Lu, Kuang-hui
      4                       Pang, Kevin
      5      (ii) TITLE OF INVENTION: Methods and Reagents for Treating
      6                              Glucose Metabolic Disorders
      7     (iii) NUMBER OF SEQUENCES: 3
      9      (iv) CORRESPONDENCE ADDRESS:
     10           (A) ADDRESSEE: Foley, Hoag & Eliot
     11           (B) STREET: One Post Office Square
     12           (C) CITY: Boston
     13           (D) STATE: MA
     14           (E) COUNTRY: USA
     15           (F) ZIP: 02109
     16       (v) COMPUTER READABLE FORM:
     17           (A) MEDIUM TYPE: Floppy disk
     18           (B) COMPUTER: IBM PC compatible
     19           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     20           (D) SOFTWARE: ASCII (text)
     21      (vi) CURRENT APPLICATION DATA:
C--> 22           (A) APPLICATION NUMBER: US/09/499,526
C--> 23           (B) FILING DATE: 10-Feb-2000
     24           (C) CLASSIFICATION:
     25    (viii) ATTORNEY/AGENT INFORMATION:
     26           (A) NAME: Vincent, Matthew P.
     27           (B) REGISTRATION NUMBER: 36,709
     28           (C) REFERENCE/DOCKET NUMBER: ONV-058.01
     29      (ix) TELECOMMUNICATION INFORMATION:
     30           (A) TELEPHONE: (617) 832-1000
     31           (B) TELEFAX: (617) 832-7000
     32 (2) INFORMATION FOR SEQ ID NO: 1:
     33       (i) SEQUENCE CHARACTERISTICS:
     34           (A) LENGTH: 36 amino acids
     35           (B) TYPE: amino acid
     36           (D) TOPOLOGY: linear
     37      (ii) MOLECULE TYPE: protein
     38      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     39 Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
     40 1               5                   10                  15
     41 Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
     42             20                  25                  30
     43 Arg Gln Arg Tyr
     44             35
C--> 47 (2) INFORMATION FOR SEQ ID NO: 2:
     48       (i) SEQUENCE CHARACTERISTICS:
     49           (A) LENGTH: 582 base pairs
     50           (B) TYPE: nucleic acid
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/499,526

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Input Set : A:\Pto.amc
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```
     51          (C) STRANDEDNESS: not relevant
W--> 52          (D) TOPOLOGY: not relevant
     53      (ii) MOLECULE TYPE: cDNA
     54      (ix) FEATURE:
     55          (A) NAME/KEY: CDS
     56          (B) LOCATION: 81..371
     57      (ix) FEATURE:
     58          (A) NAME/KEY: sig_peptide
     59          (B) LOCATION: 81..164
     60      (ix) FEATURE:
     61          (A) NAME/KEY: mat_peptide
     62          (B) LOCATION: 165..371
     63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
     64 CAGCTTGACC TGCGGCAGTG CAGCCCTTGG GACTTCCCTC GCCTTCCACC TCCTGCTCGT        60
     65 CTGCTTCACA AGCTATCGCT ATG GTG TTC GTG CGC AGG CCG TGG CCC GCC          110
     66                     Met Val Phe Val Arg Arg Pro Trp Pro Ala
     67                     -28             -25                 -20
     68 TTG ACC ACA GTG CTT CTG GCC CTG CTC GTC TGC CTA GGG GCG CTG GTC       158
     69 Leu Thr Thr Val Leu Leu Ala Leu Leu Val Cys Leu Gly Ala Leu Val
     70         -15             -10             -5
     71 GAC GCC TAC CCC ATC AAA CCC GAG GCT CCC GGC GAA GAC GCC TCG CCG       206
     72 Asp Ala Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro
     73         1           5               10
     74 GAG GAG CTG AAC CGC TAC TAC GCC TCC CTG CGC CAC TAC CTC AAC CTG       254
     75 Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu
     76   15          20              25              30
     77 GTC ACC CGG CAG CGG TAT GGG AAA AGA GAC GGC CCG GAC AGG CTT CTT       302
     78 Val Thr Arg Gln Arg Tyr Gly Lys Arg Asp Gly Pro Asp Arg Leu Leu
     79         35              40              45
     80 TCC AAA ACG TTC TTC CCC GAC GGC GAG GAC CGC CCC GTC AGG TCG CGG       350
     81 Ser Lys Thr Phe Phe Pro Asp Gly Glu Asp Arg Pro Val Arg Ser Arg
     82         50              55              60
     83 TCG GAG GGC CCA GAC CTG TGG TGAGGACCCC TGAGGCCTCC TGGGAGATCT          401
     84 Ser Glu Gly Pro Asp Leu Trp
     85         65
     86 GCCAACCACG CCCACGTCAT TTGCATACGC ACTCCCGACC CCAGAAACCC GGATTCTGCC       461
     87 TCCCGACGGC GGCGTCTGGG CAGGGTTCGG GTGCGGCCCT CCGCCCGCGT CTCGGTGCCC       521
     88 CCGCCCCCTG GGCTGGAGGG CTGTGTGTGG TCCTTCCCTG GTCCCAAAAT AAAGAGCAAA       581
     89 T                                                                     582
C--> 90 (2) INFORMATION FOR SEQ ID NO: 3:
     91      (i) SEQUENCE CHARACTERISTICS:
     92          (A) LENGTH: 97 amino acids
     93          (B) TYPE: amino acid
     94          (D) TOPOLOGY: linear
     95      (ii) MOLECULE TYPE: protein
     96      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
     97 Met Val Phe Val Arg Arg Pro Trp Pro Ala Leu Thr Thr Val Leu Leu
     98 -28         -25                 -20             -15
     99 Ala Leu Leu Val Cys Leu Gly Ala Leu Val Asp Ala Tyr Pro Ile Lys
```

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PATENT APPLICATION:  US/09/499,526       TIME: 13:17:01

Input Set : A:\Pto.amc
Output Set: N:\CRF3\12062000\I499526.raw

100          -10                  -5                  1
101 Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr
102    5              10                15                20
103 Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
104             25              30                35
105 Gly Lys Arg Asp Gly Pro Asp Arg Leu Leu Ser Lys Thr Phe Phe Pro
106             40              45                50
107 Asp Gly Glu Asp Arg Pro Val Arg Ser Arg Ser Glu Gly Pro Asp Leu
108             55              60                65
109 Trp
```

VERIFICATION SUMMARY   DATE: 12/06/2000
PATENT APPLICATION: US/09/499,526   TIME: 13:17:02

Input Set : A:\Pto.amc
Output Set: N:\CRF3\12062000\I499526.raw

L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:47 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:52 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2, Value=[not relevant]
L:90 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]